

TELEPHONE: 317-276-3334  
TELEFAX: 317-276-3861  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1353 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1353  
US-08-843-309-1

Alignment Scores:

Pred. No.: 1,876-55 Length: 1353  
Score: 586.50 Matches: 162  
Percent Similarity: 52.928 Conservative: 83  
Best Local Similarity: 34.998 Mismatches: 177  
Query Match: 25.958 Indels: 41  
DB: 2 Gaps: 14

US-09-701-229-2 (1-448) x US-08-843-309-1 (1-1353)

App: 7 Asphsphaery-----llevalvalglyleuglyysserglymetserleu 22  
Db 13 GATCATATTAAATAGAAAGTCTGTGTTAGTTGGCCAGTGTGTAATCTGCA 72  
23 Valarglyrleualargglyleuprophealavalaspthrarg----- 39  
Db 73 GCTCTTTGTTGGACAGCTGAGTCCATGTGACAGTAATGAGGAAACCTTTGCGAG 132  
40 Gluasnprogluleualathrleuarargalagintyrproglivalgluvalargcys 59  
Db 133 GACATTCACAGCGCCCAAGTTGCTGGA-----GAAGGATCAAGTCTTACA 183  
60 Glyglu-----leuaspalagluhphelucysseralarggluleu 74  
Db 184 GGTGGCATTCTTGGAACTCTTGGATGAGAGTTTGCCTTATGTTGAAAA----- 234  
75 ValserprogluleuSerleuargrhproalaleuvalalalaleuvalalaleu 94  
Db 235 ---ATTCAGGTATCCCTTACACATCCATGATGAAAGGCTTGGCCAAAGAAAT 291  
95 ArgilserglyaspIeaspleuPhealarglualalysalaproilevalalale 114  
Db 292 CCAAGTCTTGACGAGTGAATGGCTTATTTGATTTCAGAAAGCCATTTATGCTATC 351  
115 ThrglyserasnAlaLysSerThrValThrThrleuValGlygluMetAlaValAla 134  
Db 352 ACAGGATCGAACGGTAAACACCAACGACTATGATGGGAGAGTTTGGCTGCT 411  
135 AsplysargvalAlaValGlyasnleuglythrproalaleuaspIeu-----leu 152  
Db 412 GGGCAACATGCTTTTATCAGGGGATATCGGCTATCTGCCAGTCAAGTTCCTCAATA 471  
153 AlaasparilegluleuThrValleuGluleuSerPheGlnleuGluThrCysasp 172  
Db 472 GCATCAGATTAAGGACAGCTGTGTATGAACTTCTTCCAACTCATGGGTTCAA 531  
173 ArgIeuanalagluValAlaThrValleuasnValSerGluaspHismetasparg 192  
Db 532 GAATTCATCCAGATTCGCGTTATTTACCAACTCATGCCAAGTCAATGATGACAGCT 591  
193 AspglyMetAlaAspTyrHisleuAlaLysHisarglle-----PheargglyAla 209  
Db 592 GGGTCATTTTCTGAATATGATGACAGCCAAAGTGAATATCCAGAACAGATGACAGCT 651  
210 ArggluValValValaspAlaaspAlaaspAlaaspAlaaspThr--- 228  
Db 652 GATTTCCTTGCTTGAACCTTAAATCAGACTTGGCAAAAGACTTGACTTCCAAAGCAGA 711

Sequence 1  
US Pat. 5,834,270  
Hedrine et al  
Murd protein

229 -----ValproCysTrpSerPheClyleuasnLysProAspPheLysAlaPheGly 245  
Db 712 GCACTGTGTACCATTTTCAACA-----CTTGAAAGGTTCAAT-----GGA 753  
246 LeuilegluaspIygluThrleuAlaPheGlnPheaspLysleuLeuProval 265  
Db 754 GCTTATCTCGAAGATGTCAA-----CTTACTCTCCCTGTGAAAGTGTATGCGACAGC 807  
266 GlygluleuLysIleargglyValIleHisnryfserasnAlaLeuAlaValleuAla 285  
Db 808 AATGAATCGGTGTCCAGGTAGCCACATATCGAAATGGCTTCCAGCATTTCTGTA 867  
286 GlyHisAlaValGlyleupropheaspIaleuLeuGlyAlaLeuLysAlaPheSerGly 305  
Db 868 GCCAAGCTTCGTGATGTGGACAAATCAACATCAAGAAACCTTTTACGCTTGGTGT 927  
306 LeuAlaHisArgCysGlnThrValArgGluArgGlnGlyValSerTyrTyrAspAspSer 325  
Db 928 GTCAAAACACCGTCTCCAGCTTGTGATGACATCAAGGCTTTAAATCTATATACACAGCT 987  
326 LysAlaThrAsnValGlyAlaAlaLeuAlaIleGluGlyLeuGlyAlaAspIleasp 345  
Db 988 AATCACTAATATCTTGTGCTACTCAAAACCTTTATGAGATTTGAC-----AAC 1038  
346 GlyLysleuValleuLeuAlaGlyClyaspIyysglyAlaAlaPheHisaspLeuArg 365  
Db 1039 AGCAAGGTGCTGTGATGACAGGTGTGTTGGACCGTGCATCAATGATGACGAATTCG 1095  
366 GluprovalAlaArgPheCysArgAlaValValleuLeuGlyArgAspAlaGlyLeuIle 385  
Db 1096 GTGCCAGCATTTACTGACCTCAAGAAAGATGCTCATCTCGGCTCAATGCGCAAGCTGTC 1195  
386 AlaGlnAlaLeuGlyAsnAla---ValProleuValArgValAlaThrLeuAspGluAla 404  
Db 1156 AAGCGGCGACAGACAGAGCTGTGCTCTTATGTGGAGCGACAGATATTGCGATGCG 1215  
405 ValarglinalaIleGluLeuAlaArgGlnGlyaspAlaValleuLeuSerProalacys 424  
Db 1216 ACCCGCAAGGCTATGACCTTGCAGCTCAAGAGATGGTGTCTTCTTACGCTCGCCAA 1275  
425 AlaSerleuAspMetPheLysAsnPheGlnleuArgGlyArgleuPheAlaValAla 444  
Db 1276 GCCAGCTGGATATGTATGCTAATGAACTACCTGGCGACCTCTTATTCGACACAGTA 1335  
445 GluGluLeu 447  
Db 1336 GCGGAGTTA 1344

Search completed: August 14, 2003, 09:37:52  
Job time: 1636 sec

SEQ ID 2

ALIGNMENTS

RESULT 1

US-09-252-991A-7702

Sequence 7702, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 7702

LENGTH: 1371

TYPE: DNA

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-7702

Alignment Scores:

Pred. No.:

0

Score:

448.00

Percent Similarity:

100.00%

Best Local Similarity:

100.00%

Query Match:

100.00%

DB:

4

Length:

1371

Matches:

448

Conservative:

0

Mismatches:

0

Indels:

0

Gaps:

0

US-09-701-229-2 (1-448) x US-09-252-991A-7702 (1-1371)

Qy

1 MetSerLeuIleAlaSerAspHisPheArgIleValValGlyLeuGlyLysSerGlyMet 20

Db

25 ATGAGCCTGATCGCTCCGACCACTTCCGCATCGTTGTCGGCCTCGGCAAGAGCGGCATG 84

Applicant

Issued Patent





FILE REFERENCE: 107196.136  
 CURRENT APPLICATION NUMBER: US/09/252,991A  
 CURRENT FILING DATE: 1999-02-18  
 PRIOR APPLICATION NUMBER: US 60/074,788  
 PRIOR FILING DATE: 1998-02-18  
 PRIOR APPLICATION NUMBER: US 60/094,190  
 PRIOR FILING DATE: 1998-07-27  
 NUMBER OF SEQ ID NOS: 33142  
 SEQ ID NO 7928  
 LENGTH: 564  
 TYPE: DNA  
 ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-7928

Alignment Scores:  
 Pred. No.: 1.26e-115 Length: 564  
 Score: 127.00 Matches: 127  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 28.35% Indels: 0  
 Caps: 0

US-09-701-229-2 (1-448) x US-09-252-991A-7928 (1-564)

OY 322 TYRASPSPERLYSALATIRASVALGLYALALALEUALAALIEGLUGLYLEUGLY 341  
 DB 563 TAGACGATTCACAAAGCCACCAACGTCGCGCGCGCGGATCGAGGGGCTGGT 504  
 OY 342 ALASPILASPOLYLYSLEUALLEUALAGLYLYLSPOLYLYSGLYALASPHE 361  
 DB 503 GCCACATCGACGCGCAACGCTGCTCTCGCGCGCGAGACGGAAGGGCGGATTC 444  
 OY 362 HISAPLEUARGGIUPROVALALAIRGPHECYSARGALAVALLLEUGLYARGASP 381  
 DB 443 CATACCTCGCGCGCGCGCGCTCTCTCGCGCGGGGTGCTGCTGGCGCGAC 384  
 OY 382 ALACYLEULLEALAGINALALEUGLYASNALAVAPROLEUVALARGVALALATHLEU 401  
 DB 383 GCCGGCGATTGGCCAGCGACCTGCGCAACGCGTACCGCTGCTGCGCAACCTG 324  
 OY 402 ASPIGUALVALARGINALALAGILEUALARGGLUGLYASPAPALAVALLLEUSER 421  
 DB 323 GACGAGAGATCGCGCGCGCGCGAGCTGCGCGCAAGCGATGCGTCTGTGTCG 264  
 OY 422 PROIACYSALASERLEUASPMECPHELYSAPNHEGLUGIARGGLYARGLEUPHEA 441  
 DB 263 CCGCGCTCGCGCGAGCTGCGCATGTCTCAAGAACTTCGAAGAACGCGCGCTGTGCC 204  
 OY 442 LYSALVALGLUGILEUALA 448  
 DB 203 AAGCGCTGAGAGAGACTACGC 183

RESULT 5  
 US-09-252-991A-7552  
 Sequence 7552, Application US/09252991A  
 Patent No. 6551795

GENERAL INFORMATION:  
 APPLICANT: Marc J. Rubenfield et al.  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 FILE REFERENCE: 107196.136  
 CURRENT APPLICATION NUMBER: US/09/252,991A  
 CURRENT FILING DATE: 1999-02-18  
 PRIOR APPLICATION NUMBER: US 60/074,788  
 PRIOR FILING DATE: 1998-02-18  
 PRIOR APPLICATION NUMBER: US 60/094,190  
 PRIOR FILING DATE: 1998-07-27  
 NUMBER OF SEQ ID NOS: 33142  
 SEQ ID NO 7552  
 LENGTH: 360  
 TYPE: DNA  
 ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-7552

Alignment Scores:  
 Pred. No.: 5.84e-108 Length: 360  
 Score: 119.00 Matches: 119  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 26.56% Indels: 0  
 Gaps: 0

US-09-701-229-2 (1-448) x US-09-252-991A-7552 (1-360)

OY 5 ALASERAPHSIPHEARGILEVALGLYLEUGLYLYSERGLYMETSERLEUVALARG 24  
 DB 3 GCCTCGACCATCTCGCATCTGTGCGCTCGGACGAGCGCATGCTCTGTGGCC 62  
 OY 25 TYRLEUALARGGLYLEUPROPHLEALVALASPTRHARGIUALSPROFGLU 44  
 DB 63 TACCTGGCGCGCGCGCGCTTGTGCGCTTGTGATACCGAGAACCGCGGAG 122  
 OY 45 LEUALATHLEUARGALAGINTRYPROGINVALGLUALARGCYGGLYGLUEUALA 64  
 DB 123 CTGGCACCTCGCTGCTCCAGATCCGAGGAGAGTGTGCGCGCATCTGACGCGC 182  
 OY 65 GLUPHEUCYSERALARGLULEUARYVALSERPROGLYLEUSERLEUARGTHPRO 84  
 DB 183 GAGTCTCTCTCTCTCGCGCGCGCACTCTACCTACGCGCGCTGTGCGCACCGCC 242  
 OY 85 ALALEUVALGINALALALALYGLYVALARGILESERGLYASPILEASPHEUALA 104  
 DB 243 GCGCTGTACAGCGCGCGCGGAGAGTGCGCATCTCGGTGATCATCTCTGCGCC 302  
 OY 105 ARGILUALALYALAPROILEVALALALIEHLYSERASNALALYSETHVAL 123  
 DB 303 CGCGAGCGGAGCGCGCGATCTGCGCATCTCCAGCGGTTCCAGCGAAGACACCGTG 359

RESULT 6  
 US-09-252-991A-7624  
 Sequence 7624, Application US/09252991A  
 Patent No. 6551795

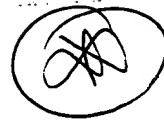
GENERAL INFORMATION:  
 APPLICANT: Marc J. Rubenfield et al.  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 FILE REFERENCE: 107196.136  
 CURRENT APPLICATION NUMBER: US/09/252,991A  
 CURRENT FILING DATE: 1999-02-18  
 PRIOR APPLICATION NUMBER: US 60/074,788  
 PRIOR FILING DATE: 1998-02-18  
 PRIOR APPLICATION NUMBER: US 60/094,190  
 PRIOR FILING DATE: 1998-07-27  
 NUMBER OF SEQ ID NOS: 33142  
 SEQ ID NO 7624  
 LENGTH: 1359  
 TYPE: DNA  
 ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-7624

Alignment Scores:  
 Pred. No.: 2.22e-56 Length: 1359  
 Score: 67.00 Matches: 67  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 14.96% Indels: 0  
 Gaps: 0

US-09-701-229-2 (1-448) x US-09-252-991A-7624 (1-1359)

OY 382 ALAGYLEULLEALAGINALALEUGLYASNALAVAPROLEUVALARGVALALATHLEU 401  
 DB 2 GCCGGCGATTGGCCAGCGCATCTGGCAACGCGGTGCTGCGCGCAACGCTG 61  
 OY 402 ASPIGUALVALARGINALALAGILEUALARGGLUGLYASPAPALAVALLLEUSER 421

SEQ ID 1



RESULT 1  
 US-09-252-991A-7861/c  
 ; Sequence 7861, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 107196.136  
 ; CURRENT APPLICATION NUMBER: US/09/252,991A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO 7861  
 ; LENGTH: 1401  
 ; TYPE: DNA  
 ; ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-7861

Query Match 81.6%; Score 1183; DB 4; Length 1401;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 1383; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy	2	GTGCTGATCGGCCTCGCCACCTTGAAGCTGCGTTGAGGACGAAGAGAGCATGAGCCTGAT	61
Db	1387	GTGCTGATCGGCCTCGCCACCTTGAAGCTGCGTTGAGGACGAAGAGAGCATGAGCCTGAT	1328
Qy	62	CGCCTCCGACCACTTCCGCATCGTTGTCGGCCTCGGCAAGAGCGGCATGTCCCTGGTGCG	121
Db	1327	CGCCTCCGACCACTTCCGCATCGTTGTCGGCCTCGGCAAGAGCGGCATGTCCCTGGTGCG	1268
Qy	122	CTACCTGGCGCGCCGCGGCTTGCCTTTTCGCCGTGGTCGATACCCGAGAGAACCCGCCGGA	181
Db	1267	CTACCTGGCGCGCCGCGGCTTGCCTTTTCGCCGTGGTCGATACCCGAGAGAACCCGCCGGA	1208
Qy	182	GCTGGCCACCCTGCGTGCCAGTATCCGCAGGTGGAAGTGCCTTGCGGCGAACTCGACGC	241
Db	1207	GCTGGCCACCCTGCGTGCCAGTATCCGCAGGTGGAAGTGCCTTGCGGCGAACTCGACGC	1148
Qy	242	CGAGTTCCTCTGCTCCGCCCGCGAACTCTACGTCAGCCCCGGCTTGTGCTGCGCACCCC	301
Db	1147	CGAGTTCCTCTGCTCCGCCCGCGAACTCTACGTCAGCCCCGGCTTGTGCTGCGCACCCC	1088
Qy	302	TGCGCTGGTACAGGCCCGCGGAAAGGCGTGCATCTCCGGTGACATCGATCTCTTCGC	361
Db	1087	CGCGCTGGTACAGGCCCGCGGAAAGGCGTGCATCTCCGGTGACATCGATCTCTTCGC	1028

362 CCGGAGGCGAAGGCCCCGATGCTGCGCATACCGGGTTCACACGGGAAGACACCGTGAC 421  
1027 CCGGAGGCGAAGGCCCCGATGCTGCGCATACCGGGTTCACACGGGAAGACACCGTGAC 968  
422 CACCTGGTGGGCGAATGGGGTGGGGCGGAGCAAGGCTGTCCCGCTGGCGGCAACT 481  
967 CACCTGGTGGGCGAATGGGGTGGGGCGGAGCAAGGCTGTCCCGCTGGCGGCAACT 908  
482 CCGGAGGCGGCGCTGCACTGCTGGCGGAGACATCAGCTGTACGTTGGAGCTGTC 541  
907 CCGGAGGCGGCGCTGCACTGCTGGCGGAGACATCAGCTGTACGTTGGAGCTGTC 848  
542 GAGCTTCCAGCTGGAACCTCGATCGCTTCACGCGGAGGTGGCGACCGCTGTAACGT 601  
847 GAGCTTCCAGCTGGAACCTCGATCGCTTCACGCGGAGGTGGCGACCGCTGTAACGT 788  
602 CAGGGAACACATATGATTCGCTACGACGGATGGCTGTACCACTGGCCAAAGCACCG 661  
787 CAGGGAACACATATGATTCGCTACGACGGATGGCTGTACCACTGGCCAAAGCACCG 728  
662 GATCTTCGCGGTGCGCCGCGAGTGTGATCGGATCGGCGATGGCGCTGACCGCGCT 721  
727 GATCTTCGCGGTGCGCCGCGAGTGTGATCGGATCGGCGATGGCGCTGACCGCGCT 668  
722 GATCGCGGATACCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 781  
667 GATCGCGGATACCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 608  
782 CCGGCTGATTCAGGAAGACGGCGCAAGAGTGGCTGGCTGCTGCTGCTGCTGCTGCT 841  
607 CCGGCTGATTCAGGAAGACGGCGCAAGAGTGGCTGGCTGCTGCTGCTGCTGCTGCT 548  
842 GGTTCGCAAGTGAAGATCCGTGGCGGCGCCACACATATTCACAGCGGCGCGCGGCTG 901  
547 GGTTCGCAAGTGAAGATCCGTGGCGGCGCCACACATATTCACAGCGGCGCGGCTG 488  
902 GCTGGGCGCATCGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 961  
487 GCTGGGCGCATCGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 428  
962 CCGGCTGCTGATGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1021  
427 CCGGCTGCTGATGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 368  
1022 TTCCAAGGCGCAACAGCTGCGCGCGCGCGCTGGCGGATCGAGGGGCTGGGTCGCGCAT 1081  
367 TTCCAAGGCGCAACAGCTGCGCGCGCGCGCTGGCGGATCGAGGGGCTGGGTCGCGCAT 308  
1082 CGACGGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1141  
307 CGACGGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 248  
1142 GCGGAGCGCGGTGCGCGCGCTGCTGCGGGGGGTGCTGCTGCTGCTGCTGCTGCTGCT 1201  
247 GCGGAGCGCGGTGCGCGCGCTGCTGCGGGGGGTGCTGCTGCTGCTGCTGCTGCTGCT 188  
1202 GATTGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1261  
187 GATTGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 128  
1262 AGTCCGGAAGGCGCGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1321  
127 AGTCCGGAAGGCGCGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 68  
1322 CCGGAGGCTGGAACATGTTCAAGAACTTCGAAGAACGCGGACGCTGTTCCCAAGCGCT 1381  
67 CCGGAGGCTGGAACATGTTCAAGAACTTCGAAGAACGCGGACGCTGTTCCCAAGCGCT 8  
1382 AGAGGAG 1388  
7 AGAGGAG 1

RESULT 2  
US-09-252-991A-7702  
; Sequence 7702, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 3142  
; SEQ ID NO 7702  
; LENGTH: 1371  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-7702

Query Match 80.5%; Score 1167; DB 4; Length 1371;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1367; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

27 AGCTGCTGAGCAGCAGAGACATGACCTGATGCTGCGAGCTACTTCCGATCGTT 86  
1 AGCTGCTGAGCAGCAGAGACATGACCTGATGCTGCGAGCTACTTCCGATCGTT 60  
87 GTGGGCGTGGCAGAGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 146  
61 GTGGGCGTGGCAGAGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
147 TTGCGCGTGTGATACCCGAGAGAACCCCGGAGCTGGCCACCTGCTGCTGCTGCT 206  
121 TTGCGCGTGTGATACCCGAGAGAACCCCGGAGCTGGCCACCTGCTGCTGCTGCT 180  
207 CCGCAGGTGGAAGTGGCTTGGCGGAACTGACCCGAGTTCCTGCTGCTGCTGCTGCT 266  
181 CCGCAGGTGGAAGTGGCTTGGCGGAACTGACCCGAGTTCCTGCTGCTGCTGCTGCT 240  
267 CTTATGTCAGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 326  
241 CTTATGTCAGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
327 GCGGTGGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 386  
301 GCGGTGGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
387 GCGATACCGGTCGCAACCGGAGAGACACCTGATACCACTGCTGCTGCTGCTGCTGCT 446  
361 GCGATACCGGTCGCAACCGGAGAGACACCTGATACCACTGCTGCTGCTGCTGCTGCT 420  
447 GCGCGGAGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 506  
421 GCGCGGAGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
507 GCGGAGCAATGAGCTGTAAGTGTGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 566  
481 GCGGAGCAATGAGCTGTAAGTGTGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
567 CCGCTAACCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 626  
541 CCGCTAACCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
627 GAGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 686  
601 GAGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
687 GTGCTGAATGCGCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 746  
661 GTGCTGAATGCGCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720

Query Match	39.1%;	Score 567;	DB 4;	Length 567;
Best Local Similarity	100.0%;	Pred. No. 1e-251;		
Matches 567;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
772	TCNAGGCTTCGAGCCATGATCGAGAGACGCCAGAGTGGCTGCGCTTCACGTTCCACA	831		

Query Match	30.2%	Score 438	DB 4	Length 564
Best Local Similarity	100.0%	Pred. NO. 2.5e-192		
Matches 438	Conservative	0	Mismatches 0	Indels 0
			Gaps	0
QY	1013	CTACGACGATTCACAAGCCACCAACTCGCGCGCCCTGCGCGCCATCGAGGGCTGG	107	
Db	564	CTACGACGATTCACAAGCCACCAACTCGCGCGCCCTGCGCGCCATCGAGGGCTGG	505	
QY	1073	TGCGACATCGACGCGCAAGCTGTGCTGCTCCGCGCGAGACGCCAAGGGCGCATTT	113	
Db	504	TGCGACATCGACGCGCAAGCTGTGCTGCTCCGCGCGAGACGCCAAGGGCGCATTT	445	



Query Match	17.8%	Score 258	DB 4	Length 1359
Best Local Similarity	100.0%	Prod. No.	1.6e-109	
Matches	258	Conservative	0	Mismatches 0; Indels 0; Gaps 0;
QY	1193	CGCCGGCTGATTGGCCAGGCACTGGGCCAAGCGCGGTACCGCTGTGCGCGTGGCAAGCT	1255	
Db	1	CGCCGGCTGATTGGCCAGGCACTGGGCCAAGCGCGGTACCGCTGTGCGCGTGGCAAGCT	60	
QY	1253	GGAGGAACACATCCGGCGGCGCGCGGCGGACCTGGCCCGCCGAAGCGATGCGGTGTGTGTC	1312	
Db	61	GGAGGAACACATCCGGCGGCGCGCGGCGGACCTGGCCCGCCGAAGCGATGCGGTGTGTGTC	120	
QY	1313	GCCGGCTGCCCGAGGCTGCACATGTTCCAAAGACTTCCAAAGAACGCGGAGCGCTGTTGCG	1372	
Db	121	GCCGGCTGCCCGAGGCTGCACATGTTCCAAAGACTTCCAAAGAACGCGGAGCGCTGTTGCG	180	
QY	1373	CAAGCGCGTAGAGAGCTAGCGCTATGCTGCGGTGTGGCGCCCTTCGGTGGCGCGTG	1432	
Db	181	CAAGCGCGTAGAGAGCTAGCGCTATGCTGCGGTGTGGCGCCCTTCGGTGGCGCGTG	240	
QY	1433	TTGAGCCGCGCAGCGGATC	1450	
Db	241	TTGAGCCGCGCAGCGGATC	258	

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Query Match Similarity      8.3%; Score 120; DB 4; Length 1170;
Best Local Similarity      100.0%; Pred. No. 5.5e-46;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      2  GGGCGAGCCGCCGCCACCTTGAACCTGCGTTGAGAGCAAGAGCATGAGCGCTGAT 61
      |||
120  GGGCGAGCCGCCGCTGGCACCTTGAACCTGCGTTGAGAGCAAGAGCATGAGCGCTGAT 61

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PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 12452  
LENGTH: 414  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-12452

Query Match  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 821 CCAAGTCGACAGCTGCTG 839  
DB 255 CCAAGTCGACAGCTGCTG 237

RESULT 13  
US-09-252-991A-8304  
Sequence 8304, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
PRIOR FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 8304  
LENGTH: 489  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-8304

Query Match  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 821 CCAAGTCGACAGCTGCTG 839  
DB 423 CCAAGTCGACAGCTGCTG 441

RESULT 14  
US-09-072-596-263  
Sequence 263, Application US/09072596  
Patent No. 6458366  
GENERAL INFORMATION:  
APPLICANT: Reed, Steven G.  
APPLICANT: Skelky, Yasir A.W.  
APPLICANT: Dillon, David C.  
APPLICANT: Campos-Neto, Antonia  
APPLICANT: Houghton, Raymond  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Twardzik, Daniel R.  
APPLICANT: Lodes, Michael J.  
APPLICANT: Hendrickson, Ronald C.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TUBERCULOSIS  
NUMBER OF SEQUENCES: 350  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/072,596  
FILING DATE: 05-MAY-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: MAKI, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.417C9  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 682-6031  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 263:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 522 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-09-072-596-263

Query Match  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1082 CGACGGCAGCTGCTGCTG 1100  
DB 429 CGACGGCAGCTGCTGCTG 447

RESULT 15  
US-09-252-991A-13195  
Sequence 13195, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
PRIOR FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 13195  
LENGTH: 723  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-13195

Query Match  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 821 CCAAGTCGACAGCTGCTG 839  
DB 216 CCAAGTCGACAGCTGCTG 234

Search completed: August 14, 2003, 07:06:19  
Job time: 117 secs

RESULT 9

US-09-557-884-1

; Sequence 1, Application US/09557884  
; Patent No. 6506581

GENERAL INFORMATION:

APPLICANT: Fleischmann et al.

TITLE OF INVENTION: The Nucleotide sequence of  
the Haemophilus influenzae Rd Genome, Fragments  
Thereof, and Uses Thereof

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: MD

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch diskette

COMPUTER: Dell Pentium

OPERATING SYSTEM: MS DOS v6.22

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/557,884

FILING DATE: 25-Apr-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/476,102

FILING DATE: JUN-5-1995

ATTORNEY/AGENT INFORMATION:

NAME: Michelle S. Marks

REGISTRATION NUMBER: 41,971

REFERENCE/DOCKET NUMBER: PB186P3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 301-309-8504

TELEFAX: 301-309-8439

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1830121 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-557-884-1

Alignment Scores:

rr. 1.000

0.212

Length:

1830121

Score:

14.00

Matches:

14

Percent Similarity:

100.00%

Conservative:

0

Best Local Similarity:

100.00%

Mismatches:

0

Query Match:

3.12%

Indels:

0

DB:

4

Gaps:

0

US-09-701-229-2 (1-448) x US-09-557-884-1 (1-1830121)

Oy

157 GluLeuTyrValLeuGluLeuSerSerPheGlnLeuGluThr 170

Db

1203588 GAACCTTTATGTACTAGAGCTTTCTAGTTTTCAGCTTGAGACA 1203629

RESULT 10

US-09-643-990A-1

; Sequence 1, Application US/09643990A

; Patent No. 6528289

GENERAL INFORMATION:

~~polypeptide~~  
polypeptide  
with identity  
to SEQID1  
fragment  
and comprises  
> 25 NA of  
SEQID1  
+ encodes an  
amino  
acid  
sequence  
of SEQID2.